Hunt
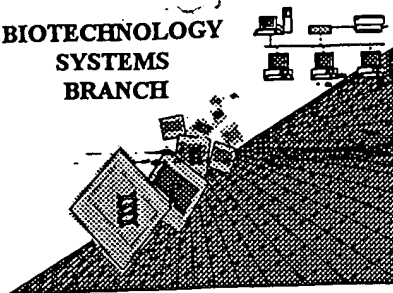
RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/506,079 A_

Source: _1642_

Date Processed by STIC: _9-28-00_

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TECH CENTE:

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED   SUGGESTED   CORRECTION   SERIAL NUMBER: _09/506,079A_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics

The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos

The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length

The rules require that a line not exceed 72 characters in length. This includes spaces.

4 ✓ Misaligned Amino Acid
         Numbering

The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII

This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences
         (OLD RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences
         (NEW RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's
          (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism
          (NEW RULES)

Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature
          (NEW RULES)

Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

J. Hunt

1642

```
        RAW SEQUENCE LISTING            DATE: 09/28/2000
        PATENT APPLICATION:  US/09/506,079A    TIME: 11:04:01

        Input Set : A:\SEQUENCE.txt
        Output Set: N:\CRF3\09282000\I506079A.raw

        SEQUENCE LISTING
    2 (1) GENERAL INFORMATION:
C--> 4     (i) APPLICANT: Clinton, Gail M., Doherty, Joni Kristin, and Adelman, John P.
    6     (ii) TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS
    8    (iii) NUMBER OF SEQUENCES: 10
   10     (iv) CORRESPONDENCE ADDRESS:
   11         (A) ADDRESSEE: DAVIS WRIGHT TREMAINE
   12         (B) STREET: 1501 Fourth Avenue, 2600 Century Square
   13         (C) CITY: Seattle
   14         (D) STATE: Washington
   15         (E) COUNTRY: U.S.A.
   16         (F) ZIP: 98101
   18     (v) COMPUTER READABLE FORM:
   19         (A) MEDIUM TYPE: Floppy disk
   20         (B) COMPUTER: PC compatible
   21         (C) OPERATING SYSTEM: Windows95
   22         (D) SOFTWARE: Word
   24     (vi) CURRENT APPLICATION DATA:
C--> 25         (A) APPLICATION NUMBER: US/09/506,079A
C--> 26         (B) FILING DATE: 16-Feb-2000
   27         (C) CLASSIFICATION:
   29    (viii) ATTORNEY/AGENT INFORMATION:
   30         (A) NAME: Oster, Jeffrey B.
   31         (B) REGISTRATION NUMBER: 32,585
   32         (C) REFERENCE/DOCKET NUMBER: 49321-1
   34     (ix) TELECOMMUNICATION INFORMATION:
   35         (A) TELEPHONE: 206 628 7711
   36         (B) TELEFAX: 206 628 7699
```

Does Not Comply Corrected Diskette Needed

RECEIVED

OCT 13 2000

TECH CENTER 1600/2900

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ERRORED SEQUENCES

   59 (2) INFORMATION FOR SEQ ID NO: 2:
   61     (i) SEQUENCE CHARACTERISTICS:     see bottom of next page
   62         (A) LENGTH: (418)
   63         (B) TYPE: amino acid
   64         (C) STRANDEDNESS: single
   65         (D) TOPOLOGY: unknown
   66     (ii) MOLECULE TYPE: polypeptide
   67     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
   69 Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu
   70               5                   10                  15
   71 Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Cys Lys
E--> 72           20 20              25 25              30 30
   73 Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
E--> 74      35 35              40 40              45 45
   75 Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
           50              55              60
```

} misaligned amino acid numbering. See #4 on Error Summary Sheet

Best Available Copy

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                RAW SEQUENCE LISTING              DATE: 09/28/2000
                PATENT APPLICATION:  US/09/506,079A    TIME: 11:04:01

                Input Set : A:\SEQUENCE.txt
                Output Set: N:\CRF3\09282000\I506079A.raw

E--> 76            50              55              60
     77 Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
E--> 78  65 68            70 70            75 75            80
     79 Gln Gly Tyr Val Leu Cys Ala His Asn Gln Val Arg Gln Val Pro Leu
E--> 80 80              85              90              95
     81 Gln Arg Leu Arg Ile Val Arg Gly Thr Leu Phe Glu Asp Asn Tyr
E--> 82              100             105             110
     83 Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Arg Arg Thr Thr Pro
E--> 84              115             120             125
     85 Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
E--> 86              130             135             140
     87 Leu Thr Glu Cys Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
E--> 88          145             150             155
     89 Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
E--> 90 160             165             170             175
     91 Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
E--> 92              180             185             190
     93 His Pro Cys Ser Pro Cys Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
E--> 94              195             200             205
     95 Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
E--> 96              210             215             220
     97 Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
E--> 98          225             230             235
     99 Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
E--> 100 240             245             250             255
     101 His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
E--> 102             260             265             270
     103 Thr Tyr Asn Thr Asp Thr Phe Glu Ser Cys Pro Asn Pro Glu Gly Arg
E--> 104             275             280             285
     105 Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Lys Leu
E--> 106         290             295             300
     107 Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
E--> 108         305             310             315
     109 Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
E--> 110 320             325             330             335
W--> 111 Pro Cys Ala Arg Val Gly Xaa His Ser Xaa Pro Arg Pro Ala Ala
E--> 112             340             345             350
W--> 113 Val Pro Val Pro Xaa Arg Xaa Gln Pro Xaa Pro Ala His Pro Val Leu
E--> 114             355             360             365
W--> 115 Ser Phe Leu Arg Pro Ser Trp Asp Xaa Val Ser Ala Phe Tyr Ser Leu
E--> 116         370             375             380
W--> 117 Pro Leu Ala Pro Leu Asp Pro Thr Ser Val Xaa Ile Ser Pro Val Ser
E--> 118         385             390             395
W--> 119 Val Gly Arg Gly Xaa Asp Pro Asp Ala His Val Ala Val Xaa Leu Ser
E--> 120 400             405             410             415
E--> 121 Arg Tyr Glu Gly
```

(handwritten annotations) misaligned amino acid numbering

420 amino acids shown
418 listed as length

VERIFICATION SUMMARY   DATE: 09/28/2000
PATENT APPLICATION: US/09/506,079A TIME: 11:04:02

Input Set : A:\SEQUENCE.txt
Output Set: N:\CRF3\09282000\I506079A.raw

L:4 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]
L:25 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:26 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:45 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1, Value=[HER-2 ECD
antagonist]
L:48 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:50 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:54 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:56 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:72 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2
L:111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:115 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:117 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:121 M:203 E: No. of Seq. differs, LENGTH:Input:418 Found:420 SEQ:2
L:130 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3, Value=
[oligonucleotide]
L:142 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4, Value=
[oligonucleotide]
L:153 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5, Value=
[oligonucleotide]
L:165 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6, Value=
[oligonucleotide]
L:176 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7, Value=
[oligonucleotide]
L:187 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8, Value=
[oligonucleotide]
L:198 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9, Value=
[oligonucleotide]
L:209 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10, Value=[DNA]
L:213 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:221 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:225 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10.
L:229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10

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